MONTANA FISH, WILDLIFE & PARKS
FINAL PROJECT PERFORMANCE REPORT

GRANT TITLE: **Montana Sauger Genetic Characteristics**
AGREEMENT: **T - 7 - 1**
PERIOD COVERED: **April 1, 2003 through June 30, 2006**

Objective

The objectives of this project are to determine the extent of genetic variation in a minimum of 16 native Montana sauger sub-populations, and to determine the extent of hybridization and introgression between Montana sauger and walleye.

Location

Genetic tissue samples will be collected throughout the historic range of sauger in the Missouri River Basin (including major tributaries to the Missouri River) downstream from Great Falls, Montana and east to the Montana-North Dakota border. Samples will also be collected from populations in the Yellowstone River Basin (including major tributaries to the Yellowstone River) downstream of Billings, Montana, and northeast to the Montana-North Dakota border.

Accomplishments

Sauger specimens were collected from 21 sites; 16 sites in Montana and four sits in neighboring Wyoming and Alberta, Canada, from drainages that flow into Montana, and one site from North Dakota, downstream from Montana on the Missouri River system. Four (*mMDH-1*,PGM-1*, ALAT** and *IDDH**) diagnostic loci between saugers and walleyes and two (*sMDH-3** and *PROT-3**) informative loci in saugers were used to detect sauger-walleye hybrids. Hybrid and introgressed fish were found at 12 of the 18 sites examined after pooling to address low sample sizes at three sites. Hybridization rates ranged from 0-22% in the Missouri River drainage and 0-4% in the Yellowstone River drainage, although rates of up to 10% were observed in potential Yellowstone River brood fish, and 20.4% in Lake Sakakawea, ND. Several microsatellite loci offer potential for analysis of hybridization between walleye and sauger. Brood stock to be used for supplemental sauger stocking should be genetically screened to prevent the propagation and accidental stocking of hybrids, but a more reliable way of conducting this screening will be required.

Two (*EST** and *SOD-2**) of the 35 loci analyzed were polymorphic in Montana saugers. Montana populations showed moderate structuring (FST = 0.091) and were partitioned into two main genetic groups. These two genetic groups did not coincide with the two main river drainages, the Missouri River and Yellowstone River drainages. One of these groups consisted of fish from the Missouri River below Fort Peck Reservoir dam and the Milk River below the Fresno Reservoir dam, and fish from the Boysen Reservoir in Wyoming. The other main group contained a mixture of fish from both the Missouri River and Yellowstone River drainages. Milk River saugers from above the Fresno Reservoir dam had significantly different allele frequencies from those below the dam. Significant genetic heterogeneity was found among all of the sauger composite populations examined. Several composite populations showed significant deviations from Hardy-Weinberg expectations, all due to heterozygote deficits, likely caused by the Wahlund effect because sampling was not confined to spawning populations, something that should be avoided in future studies of genetic variation in Montana sauger. Due to the population differentiation present in Montana sauger populations, they should be managed individually and stock transfer is not recommended.

Microsatellite DNA analysis revealed a high level of genetic variability in Montana sauger populations, with most of the variation occurring within rather than among populations. Nevertheless, the Bighorn River population from Wyoming was significantly different from all of the other populations examined. Microsatellite DNA analysis offers promise for future studies on Montana sauger populations because non-lethal samples such as scales could be examined for genetic variation once DNA has been extracted from cells attached to them. This would permit a more thorough sampling of spawning populations and a possible analysis of any archived sauger scale samples to search for historic trends in genetic variation in Montana sauger.

See the CD with the entire project report titled, "Genetic Variation and Hybridization with Walleye in Montana: Sauger Populations Determined by Protein Electrophoresis and Microsatellite Analysis" for additional information.

Variances

None

Expenditure Recap

Proposed:

	Federal Share		Match		Total
Direct Costs	45,000.00		20,000.00		65,000.00
Indirect @ 20%	9,000.00				9,000.00
Total	$ 54,000.00	72.97%	$ 20,000.00	27.03%	$ 74,000.00

Actual:

	Federal Share		Match		Total
Direct Costs	44,991.00		20,000.00		64,991.00
Indirect (various rates)	8,154.41				8,154.41
Total	53,154.41	72.7%	20,000.00	27.3%	73,154.41

The non-federal share of funding came in the form of a cash contribution ($20,000) by PPL Montana toward this project, which was used to cover contracting expenses with Troy University.

Project Personnel

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